

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for preparing a plurality of different synthetic singled-stranded nucleic acids, comprising the steps:
 - (a) ~~provision of providing~~ a support with a surface which comprises a plurality of positions at each of which different nucleic acid fragments are present, comprising base sequences which are complementary to the nucleic acids to be prepared,
 - (b) ~~addition of adding~~ nucleotide building blocks and ~~of~~ an enzyme which brings about generation of different singled-stranded nucleic acids from the complementary base sequences from (a), and
 - (c) ~~detachment of detaching~~ the singled-stranded nucleic acids generated in step (b) and, where appropriate, ~~provision providing~~ for further operations.

2. (Currently Amended) A method for preparing a predetermined nucleic acid double strand, comprising the steps:
 - (a) ~~provision of providing~~ a support with a surface which comprises a plurality of positions at each of which different nucleic acid fragments are present, comprising base sequences which are complementary to partial sequences of the nucleic acid double strand to be prepared,

(b) ~~addition of adding~~ nucleotide building blocks and of an enzyme which brings about generation of singled-stranded partial sequences of the nucleic acid double strand to be prepared from the complementary base sequences from (a), and

(c) ~~assembly of assembling~~ the singled-stranded partial sequences generated in step b) to give the desired nucleic acid double strand.

3. (Previously Presented) The method as claimed in claim 1, characterized in that the support is selected from flat supports, porous supports, reaction supports with electrodes, reaction supports with particles or beads, microfluidic reaction supports which optionally have surface modifications such as gels, linkers, spacers, polymers, amorphous layers or/and 3D matrices, and combinations of the aforementioned supports.

4. (Previously Presented) The method as claimed in claim 1, characterized in that a microfluidic support is provided.

5. (Previously Presented) The method as claimed in claim 1, characterized in that the nucleic acid fragments from (a) are generated by spatially resolved *in situ* synthesis on the support.

6. (Original) The method as claimed in claim 5, characterized in that the nucleic acid fragments from (a) are synthesized by spatially or/and time-resolved illumination by means of a programmable light source matrix.

7. (Original) The method as claimed in claim 6, characterized in that the spatially or/and time-resolved synthesis takes place in a microfluidic support with one or more fluidic reaction chambers and one or more reaction zones within a fluidic reaction chamber.

8. (Previously Presented) The method as claimed in claim 2, characterized in that the assembly of the partial sequences in step (c) takes place at least partly in one or more steps on the support.

9. (Previously Presented) The method as claimed in claim 1, characterized in that the nucleic acid fragments from (a) are chosen so that the nucleic acids or partial sequences formed in step (b) can be joined to give nucleic acid double-stranded hybrids.

10. (Previously Presented) The method as claimed in claim 1, characterized in that a plurality of nucleic acids or partial sequences which form a strand of the nucleic acid double strand are covalently connected together.

11. (Original) The method as claimed in claim 10, characterized in that the covalent connection comprises a treatment with ligase or/and a filling-in of gaps in the strands with DNA polymerase.

12. (Previously Presented) The method as claimed in claim 1, characterized in that step (b) comprises the addition of at least one primer for each position of the support, the primer being complementary to part of the nucleic acid fragment located at this position and step (b) comprising an elongation of the primer.

13. (Previously Presented) The method as claimed in claim 1, characterized in that double-stranded nucleic acid fragments are provided in step (a), with at least one strand being tethered to the surface of the support.

14. (Original) The method as claimed in claim 13, characterized in that step (b) comprises transcription of double-stranded DNA fragments or/and replication of double-stranded RNA fragments.

15. (Previously Presented) The method as claimed in claim 1, characterized in that nucleic acid fragments comprising a self-priming 3' end are provided in step (a), and step (b) comprises elongation of the 3' end.

16. (Original) The method as claimed in claim 15, which comprises elimination of the elongation product.

17. (Previously Presented) The method as claimed in claim 1, characterized in that double-stranded, circular nucleic acid fragments are provided in step (a), one strand being tethered to the surface of the support, and the other strand

comprising a self-priming 3' end, and step (b) comprising elongation of the 3' end.

18. (Original) The method as claimed in claim 17, which comprises elimination of the elongation product.

19. (Previously Presented) The method as claimed in claim 1, characterized in that the nucleic acid fragments from (a) are generated by: provision of capture probes at the positions and binding of nucleic acid fragments from a fluid passed over the support to the capture probes, where the capture probes are complementary to partial regions of the nucleic acid fragments.

20. (Currently Amended) The method as claimed in claim 1, ~~characterized in that wherein~~ recognition sequences for specific interaction with molecules such as proteins, nucleic acids, peptides, drugs, saccharides, lipids, hormones or/and organic compounds are present at one or more positions in the sequence of the ~~generated nucleic acids acid or of the nucleic acid double strand.~~

21. (Currently Amended) The method as claimed in claim 1, ~~characterized in that wherein~~ the sequence of the ~~generated~~ nucleic ~~acids acid or of the nucleic acid double strands~~ is a naturally occurring sequence, a non-naturally occurring ~~occurring~~ sequence or a combination of ~~these two~~ ~~thereof~~.

22. (Previously Presented) The method as claimed in claim 1, characterized in that the sequence is taken from a database, from a sequencing experiment or from an apparatus for integrated synthesis and analysis of polymers.

23. (Previously Presented) The method as claimed in claim 1, characterized in that the nucleotide building blocks may comprise naturally occurring nucleotides, modified nucleotides or mixtures thereof.

24. (Previously Presented) The method as claimed in claim 1, characterized in that modified nucleotide building blocks are used for labeling and subsequent detection of the nucleic acids or of the joined nucleic acid double strands.

25. (Original) The method as claimed in claim 24, characterized in that molecules to be detected in a light-dependent or/and electrochemical manner are used as labeling groups.

26. (Currently Amended) The ~~use of nucleic acids or nucleic acid double strands prepared by the method as claimed in~~ method of claim 1, wherein ~~said prepared nucleic acids are tools for therapeutic or pharmacological purposes.~~

27. (Currently Amended) The ~~use of nucleic acids or nucleic acid double strands prepared by the method as claimed in~~ method of claim 1, wherein ~~said prepared nucleic acids are tools for diagnostic purposes.~~

28. (Currently Amended) The ~~use as claimed in~~ method of claim 26, further comprising a ~~transfer~~ transferring said prepared nucleic acids into effector cells.

29. (Currently Amended) The ~~use of nucleic acids or nucleic acid double~~ strands prepared by the process as claimed in method of claim 1, ~~where they~~ wherein said prepared nucleic acids are stabilized, condensed or/and topologically manipulated during a stepwise combination and joining or subsequent thereto.

30. (Currently Amended) The ~~use as claimed in~~ method of claim 29 ~~where the~~ wherein said stabilization, condensation or/and topological manipulation is effected by functional molecules such as histones or topoisomerases.

31. (Currently Amended) The ~~use of nucleic acids or nucleic acid double~~ strands prepared by the method as claimed in method of claim 1, wherein said prepared nucleic acids are propagatable cloning vectors as propagatable cloning ~~vector where the propagatable cloning vector can serve in suitable target cells for~~ ~~transcription, for expression of the transcribed sequence, and where appropriate~~ ~~for the isolation of expressed gene products.~~

32. (New) The method as claimed in claim 2, wherein recognition sequences for specific interaction with molecules selected from the group consisting of

proteins, nucleic acids, peptides, drugs, saccharides, lipids, hormones, and organic compounds are present at one or more positions in the sequence of the generated nucleic acid double strand.

33. (New) The method as claimed in claim 2, wherein the sequence of the generated nucleic acid double strand is a naturally occurring sequence, a non-naturally occurring sequence, or a combination thereof.